

F Errors Corrected by the STIC Systems Branch

PCT 09
#3

Serial Number: 09/700,687

CRF Processing Date: _____
 Edited by: _____
 Verified by: _____ (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: **ENTERED**
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Edited a format error in the <110> Applicant data section.

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form. 3/1/95

PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/700,687

DATE: 04/04/2001

TIME: 11:43:18

Input Set : A:\PTO.txt

Output Set: N:\CRF3\04042001\I700687.raw

W--> 3 <110> COMPAGNIE GERVAIS DANONE
W--> 4 GENDRE, Francois
W--> 5 BENBADIS, Laurent
W--> 6 BRIGNON, Pierre
W--> 0 <110> APPLICANT:
8 <120> TITLE OF INVENTION: MUTANT LACTOBACILLUS BULGARICUS STRAINS FREE
9 FROM BETA-GALACTOSIDASE ACTIVITY
11 <130> FILE REFERENCE: MJPCb191/143
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/700,687
C--> 14 <141> CURRENT FILING DATE: 2000-11-17
16 <150> PRIOR APPLICATION NUMBER: FR9806456
17 <151> PRIOR FILING DATE: 1998-05-22
19 <160> NUMBER OF SEQ ID NOS: 3
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 5059
25 <212> TYPE: DNA
26 <213> ORGANISM: Lactobacillus bulgaricus
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (122)..(1873)
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1877)..(4519)
36 <400> SEQUENCE: 1
37 gcttgtctca cgcttgtcgt acgcggccgg tgcctttggc aacgacgtct tctacgcgac 60
39 tctgtcaacc tactttatcg tcttcgtcac caccacctc tttaatgccg gtgaccacaa 120
41 g atg atc ttt atc atc acc aac ttg atc acc gcc atc cgg atc ggg gaa 169
42 Met Ile Phe Ile Ile Thr Asn Leu Ile Thr Ala Ile Arg Ile Gly Glu
43 1 5 10 15
45 gtc ctg ctc gac ccc ttg atc ggt aac gcc atc gac cgg acc gaa agc 217
46 Val Leu Leu Asp Pro Leu Ile Gly Asn Ala Ile Asp Arg Thr Glu Ser
47 20 25 30
49 cgg tgg ggg aag ttc aag ccc tgg gtt gtg ggc ggg ggg atc atc agc 265
50 Arg Trp Gly Lys Phe Lys Pro Trp Val Val Gly Gly Gly Ile Ile Ser
51 35 40 45
53 tca tta gcc ctc tta gcc ctc ttt acc gac ttt ggc ggc att aac caa 313
54 Ser Leu Ala Leu Leu Ala Leu Phe Thr Asp Phe Gly Gly Ile Asn Gln
55 50 55 60
57 agc aac ccc gtt gtt tac tta gta atc ttc ggt att gtt tac ttg att 361
58 Ser Asn Pro Val Val Tyr Leu Val Ile Phe Gly Ile Val Tyr Leu Ile
59 65 70 75 80
61 atg gat atc ttc tac tca ttt aaa gac act ggc ttc tgg gcc atg atc 409
62 Met Asp Ile Phe Tyr Ser Phe Lys Asp Thr Gly Phe Trp Ala Met Ile
63 85 90 95
65 ccg gcc ttg tcc ctg gat tcc cgg gaa aga gag aag acc tcc acc ttc 457
66 Pro Ala Leu Ser Leu Asp Ser Arg Glu Arg Glu Lys Thr Ser Thr Phe

*Format errors in
<110> Applicant data section.*

*Does Not Comply
Corrected Diskette Needed*

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Input Set : A:\PT0.txt

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67		100		105		110		
69	gcc aga gtc	ggc tcc acc atc	ggg gcc aac ctg gtc	ggg gta gtc atc	505			
70	Ala Arg Val	Gly Ser Thr Ile	Gly Ala Asn Leu Val	Gly Val Val Ile				
71		115		120		125		
73	acc cca atc atc	ctc ttc ttc tgc	gcc agc aag gcc aac	ccc aac ggg	553			
74	Thr Pro Ile	Ile Leu Phe Phe	Ser Ala Ser Lys	Ala Asn Pro Asn Gly				
75		130		135		140		
77	gat aag cag	ggc tgg ttc ttc	ttt gcc ttg atc	gtg gcc att gtc	ggc	601		
78	Asp Lys Gln	Gly Trp Phe Phe	Phe Ala Leu Ile	Val Ala Ile Val	Gly			
79	145		150		155		160	
81	atc ttg acc	tca att acc gtt	ggt ctt ggt act	cac gaa gta aaa	tcc	649		
82	Ile Leu Thr	Ser Ile Thr Val	Gly Leu Gly Thr	His Glu Val Lys	Ser			
83		165		170		175		
85	gcc ctg cgg	gaa agc aat gaa	aag acc act ttg	aag cag gtc ttt	aag	697		
86	Ala Leu Arg	Glu Ser Asn Glu	Lys Thr Thr Leu	Lys Gln Val Phe	Lys			
87		180		185		190		
89	gtc ctg ggg	caa aac gac cag	ctc ctc tgg ctg	gcc ttt gcc tac	tgg	745		
90	Val Leu Gly	Gln Asn Asp Gln	Leu Leu Trp Leu	Ala Phe Ala Tyr	Trp			
91		195		200		205		
93	ttt tac ggc	ctg ggt atc aac	acc ctg aac gct	ctg caa ctt tac	tac	793		
94	Phe Tyr Gly	Leu Gly Ile Asn	Thr Leu Asn Ala	Leu Gln Leu Tyr	Tyr			
95		210		215		220		
97	ttc tca tac	atc tta ggc gat	gcc cgc ggc tac	agc ctg ctt tac	acc	841		
98	Phe Ser Tyr	Ile Leu Gly Asp	Ala Arg Gly Tyr	Ser Leu Leu Tyr	Thr			
99	225		230		235		240	
101	atc aac acc	ttt gtc ggt tta	atc tct gca tcc	ttc ttc cca tca	ctg	889		
102	Ile Asn Thr	Phe Val Gly Leu	Ile Ser Ala Ser	Phe Phe Pro Ser	Leu			
103		245		250		255		
105	gcc aag aag	ttc aac aga aat	cgc ctc ttc tac	gcc tgc atc gcg	gtg	937		
106	Ala Lys Lys	Phe Asn Arg Asn	Arg Leu Phe Tyr	Ala Cys Ile Ala	Val			
107		260		265		270		
109	atg ctg tta	ggg atc ggg gtc	ttc tcc gtg gcc	agc ggt tct ctg	gcc	985		
110	Met Leu Leu	Gly Ile Gly Val	Phe Ser Val Ala	Ser Gly Ser Leu	Ala			
111		275		280		285		
113	ctg tcc ctt	gtt ggg gca gaa	ttc ttc ttt att	ccg cag cct ctg	gcc	1033		
114	Leu Ser Leu	Val Gly Ala Glu	Phe Phe Phe Ile	Pro Gln Pro Leu	Ala			
115		290		295		300		
117	ttc ctg gtc	gtt ttg atg atc	atc tct gac gct	gtt gaa tac ggc	cag	1081		
118	Phe Leu Val	Val Leu Met Ile	Ile Ser Asp Ala	Val Glu Tyr Gly	Gln			
119	305		310		315		320	
121	ctg aaa act	ggc cac aga gac	gaa gct ttg acc	ctg tct gtc cgg	cca	1129		
122	Leu Lys Thr	Gly His Arg Asp	Glu Ala Leu Thr	Leu Ser Val Arg	Pro			
123		325		330		335		
125	ttg gtc gat	aag ctg ggc ggg	gcc ttg tcc aac	tgg ttt gtt tcc	ttg	1177		
126	Leu Val Asp	Lys Leu Gly Gly	Ala Leu Ser Asn	Trp Phe Val Ser	Leu			
127		340		345		350		
129	att gcc tta	act gcc ggc atg	acc act ggg gcg	act gcc tca aca	att	1225		
130	Ile Ala Leu	Thr Ala Gly Met	Thr Thr Gly Ala	Thr Ala Ser Thr	Ile			
131		355		360		365		

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133	aca	gct	cat	ggc	cag	atg	gtc	ttc	aag	tta	gct	atg	ttt	gcc	tta	ccg	1273
134	Thr	Ala	His	Gly	Gln	Met	Val	Phe	Lys	Leu	Ala	Met	Phe	Ala	Leu	Pro	
135		370					375					380					
137	gca	gtc	atg	ctc	ttg	atc	gct	gtt	tct	att	ttc	gcc	aaa	aag	gtc	ttc	1321
138	Ala	Val	Met	Leu	Leu	Ile	Ala	Val	Ser	Ile	Phe	Ala	Lys	Lys	Val	Phe	
139	385					390					395					400	
141	ttg	act	gaa	gaa	aag	cac	gcg	gaa	atc	gtc	gac	cag	ctg	gaa	act	caa	1369
142	Leu	Thr	Glu	Glu	Lys	His	Ala	Glu	Ile	Val	Asp	Gln	Leu	Glu	Thr	Gln	
143					405					410					415		
145	ttc	agc	caa	agc	cat	gcc	caa	aag	ccg	gcg	caa	gct	gaa	agc	ttc	act	1417
146	Phe	Ser	Gln	Ser	His	Ala	Gln	Lys	Pro	Ala	Gln	Ala	Glu	Ser	Phe	Thr	
147				420					425					430			
149	ttg	gcc	agc	cca	gtc	tcc	gga	caa	tta	atg	aac	ctg	gac	atg	gtt	gac	1465
150	Leu	Ala	Ser	Pro	Val	Ser	Gly	Gln	Leu	Met	Asn	Leu	Asp	Met	Val	Asp	
151		435					440					445					
153	gac	ccg	gtc	ttt	gcc	gac	aaa	aag	tta	ggc	gac	ggc	ttt	gcc	ctg	gtg	1513
154	Asp	Pro	Val	Phe	Ala	Asp	Lys	Lys	Leu	Gly	Asp	Gly	Phe	Ala	Leu	Val	
155		450					455					460					
157	cca	gca	gac	ggt	aag	gtc	tac	gcg	cca	ttt	gcc	ggt	act	gtc	cgc	cag	1561
158	Pro	Ala	Asp	Gly	Lys	Val	Tyr	Ala	Pro	Phe	Ala	Gly	Thr	Val	Arg	Gln	
159	465				470						475					480	
161	ctg	gcc	aag	acc	cgg	cac	tcg	atc	gtc	ctg	gaa	aat	gaa	cat	ggg	gtc	1609
162	Leu	Ala	Lys	Thr	Arg	His	Ser	Ile	Val	Leu	Glu	Asn	Glu	His	Gly	Val	
163				485					490						495		
165	ttg	gtc	ttg	att	cac	ctt	ggc	ctg	ggc	acg	gtc	aaa	tta	aac	ggg	act	1657
166	Leu	Val	Leu	Ile	His	Leu	Gly	Leu	Gly	Thr	Val	Lys	Leu	Asn	Gly	Thr	
167				500					505					510			
169	ggc	ttt	gtc	agc	tat	gtt	gaa	gag	ggc	agc	cag	gta	gaa	gcc	ggc	cag	1705
170	Gly	Phe	Val	Ser	Tyr	Val	Glu	Glu	Gly	Ser	Gln	Val	Glu	Ala	Gly	Gln	
171		515						520				525					
173	cag	atc	ctg	gaa	ttc	tgg	gac	ccg	gcg	atc	aag	cag	gcc	aag	ctg	gac	1753
174	Gln	Ile	Leu	Glu	Phe	Trp	Asp	Pro	Ala	Ile	Lys	Gln	Ala	Lys	Leu	Asp	
175		530					535					540					
177	gac	acg	gta	atc	gtg	acc	gtc	atc	aac	agc	gaa	act	ttc	gca	aat	agc	1801
178	Asp	Thr	Val	Ile	Val	Thr	Val	Ile	Asn	Ser	Glu	Thr	Phe	Ala	Asn	Ser	
179	545				550						555					560	
181	cag	atg	ctc	ttg	ccg	atc	ggc	cac	agc	gtc	caa	gcc	ctg	gat	gat	gta	1849
182	Gln	Met	Leu	Leu	Pro	Ile	Gly	His	Ser	Val	Gln	Ala	Leu	Asp	Asp	Val	
183				565					570						575		
185	ttc	aag	tta	gaa	ggg	aag	aat	tag	aaa	atg	agc	aat	aag	tta	gta	aaa	1897
186	Phe	Lys	Leu	Glu	Gly	Lys	Asn			Met	Ser	Asn	Lys	Leu	Val	Lys	
W--> 187				580						585					590		
189	gaa	aaa	aga	gtt	gac	cag	gca	gac	ttg	gcc	tgg	ctg	act	gac	ccg	gaa	1945
190	Glu	Lys	Arg	Val	Asp	Gln	Ala	Asp	Leu	Ala	Trp	Leu	Thr	Asp	Pro	Glu	
W--> 191				595					600					605			
193	gtt	tac	gaa	gtc	aat	aca	att	ccc	ccg	cac	tcc	gac	cat	gag	tcc	ttc	1993
194	Val	Tyr	Glu	Val	Asn	Thr	Ile	Pro	Pro	His	Ser	Asp	His	Glu	Ser	Phe	
W--> 195			610					615				620					
197	caa	agc	cag	gaa	gaa	ctg	gag	gag	ggc	aag	tcc	agt	tta	gtg	cag	tcc	2041

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	202	Leu	Asp	Gly	Asp	Trp	Leu	Ile	Asp	Tyr	Ala	Glu	Asn	Gly	Gln	Gly	Pro	
W-->	203	640					645					650					655	
	205	gtc	aac	ttc	tat	gca	gaa	gac	ttt	gac	gat	agc	aat	ttt	aag	tca	gtc	2137
	206	Val	Asn	Phe	Tyr	Ala	Glu	Asp	Phe	Asp	Asp	Ser	Asn	Phe	Lys	Ser	Val	
W-->	207					660					665					670		
	209	aaa	gta	ccc	ggc	aac	ctg	gaa	ctg	caa	ggc	ttt	ggc	cag	ccc	cag	tat	2185
	210	Lys	Val	Pro	Gly	Asn	Leu	Glu	Leu	Gln	Gly	Phe	Gly	Gln	Pro	Gln	Tyr	
W-->	211				675					680					685			
	213	gtc	aac	gtc	caa	tat	cca	tgg	gac	ggc	agt	gag	gag	att	ttc	ccg	ccc	2233
	214	Val	Asn	Val	Gln	Tyr	Pro	Trp	Asp	Gly	Ser	Glu	Glu	Ile	Phe	Pro	Pro	
W-->	215			690					695					700				
	217	caa	att	cca	agc	aaa	aat	ccg	ctc	gct	tct	tat	gtc	aga	tac	ttt	gac	2281
	218	Gln	Ile	Pro	Ser	Lys	Asn	Pro	Leu	Ala	Ser	Tyr	Val	Arg	Tyr	Phe	Asp	
W-->	219		705				710					715						
	221	ctg	gat	gaa	gct	ttc	tgg	gac	aag	gaa	gtc	agc	ttg	aag	ttt	gac	ggg	2329
	222	Leu	Asp	Glu	Ala	Phe	Trp	Asp	Lys	Glu	Val	Ser	Leu	Lys	Phe	Asp	Gly	
W-->	223	720				725				730					735			
	225	gcg	gca	aca	gcc	atc	tat	gtc	tgg	ctg	aac	ggc	cac	ttc	gtc	ggc	tac	2377
	226	Ala	Ala	Thr	Ala	Ile	Tyr	Val	Trp	Leu	Asn	Gly	His	Phe	Val	Gly	Tyr	
W-->	227				740					745					750			
	229	ggg	gaa	gac	tcc	ttt	acc	cca	agc	gag	ttt	atg	gtt	acc	aag	ttc	ctc	2425
	230	Gly	Glu	Asp	Ser	Phe	Thr	Pro	Ser	Glu	Phe	Met	Val	Thr	Lys	Phe	Leu	
W-->	231			755				760				765						
	233	aag	aaa	gaa	aat	aac	cgc	ctg	gca	gtg	gct	ctc	tac	aag	tat	tct	tcc	2473
	234	Lys	Lys	Glu	Asn	Asn	Arg	Leu	Ala	Val	Ala	Leu	Tyr	Lys	Tyr	Ser	Ser	
W-->	235			770				775				780						
	237	gcc	tcc	tgg	ctg	gaa	gac	cag	gac	ttc	tgg	cgc	atg	tct	ggg	ttg	ttc	2521
	238	Ala	Ser	Trp	Leu	Glu	Asp	Gln	Asp	Phe	Trp	Arg	Met	Ser	Gly	Leu	Phe	
W-->	239		785				790					795						
	241	aga	tca	gtg	act	ctt	cag	gcc	aag	ccg	cgt	ctg	cac	ttg	gag	gac	ctt	2569
	242	Arg	Ser	Val	Thr	Leu	Gln	Ala	Lys	Pro	Arg	Leu	His	Leu	Glu	Asp	Leu	
W-->	243	800				805				810					815			
	245	aag	ctt	acg	gcc	agc	ttg	acc	gat	aac	tac	caa	aaa	gga	aag	ctg	gaa	2617
	246	Lys	Leu	Thr	Ala	Ser	Leu	Thr	Asp	Asn	Tyr	Gln	Lys	Gly	Lys	Leu	Glu	
W-->	247				820					825					830			
	249	gtc	gaa	gcc	aat	att	gcc	tac	cgc	ttg	cca	aat	gcc	agc	ttt	aag	ctg	2665
	250	Val	Glu	Ala	Asn	Ile	Ala	Tyr	Arg	Leu	Pro	Asn	Ala	Ser	Phe	Lys	Leu	
W-->	251			835				840				845						
	253	gaa	gtg	cgg	gat	agt	gaa	ggt	gac	ttg	ggt	gct	gaa	aag	ctg	ggc	cca	2713
	254	Glu	Val	Arg	Asp	Ser	Glu	Gly	Asp	Leu	Val	Ala	Glu	Lys	Leu	Gly	Pro	
W-->	255			850				855				860						
	257	atc	aga	agc	gag	cag	ctg	gaa	ttc	act	ctg	gct	gat	ttg	cca	gta	gct	2761
	258	Ile	Arg	Ser	Glu	Gln	Leu	Glu	Phe	Thr	Leu	Ala	Asp	Leu	Pro	Val	Ala	
W-->	259		865				870				875							
	261	gcc	tgg	agc	gcg	gaa	aag	cct	aac	ctt	tac	cag	gtc	cgc	ctg	tat	tta	2809
	262	Ala	Trp	Ser	Ala	Glu	Lys	Pro	Asn	Leu	Tyr	Gln	Val	Arg	Leu	Tyr	Leu	

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      265 tac cag gca ggc agc ctc tta gag gtt agc cgg cag gaa gtg ggt ttc 2857
      266 Tyr Gln Ala Gly Ser Leu Leu Glu Val Ser Arg Gln Glu Val Gly Phe
W--> 267                900                905                910
      269 cgc aac ttt gaa cta aaa gac ggg att atg tac ctt aac ggc cag cgg 2905
      270 Arg Asn Phe Glu Leu Lys Asp Gly Ile Met Tyr Leu Asn Gly Gln Arg
W--> 271                915                920                925
      273 atc gtc ttc aag ggg gcc aac cgg cac gaa ttt gac agt aag ttg ggc 2953
      274 Ile Val Phe Lys Gly Ala Asn Arg His Glu Phe Asp Ser Lys Leu Gly
W--> 275                930                935                940
      277 cgg gct atc aca gaa gag gat atg atc tgg gat atc aag acc atg aag 3001
      278 Arg Ala Ile Thr Glu Glu Asp Met Ile Trp Asp Ile Lys Thr Met Lys
W--> 279                945                950                955
      281 cga agc aac atc aat gct gtc cgc tgc tct cac tac ccg aac cag tcc 3049
      282 Arg Ser Asn Ile Asn Ala Val Arg Cys Ser His Tyr Pro Asn Gln Ser
W--> 283 960                965                970                975
      285 ctc ttt tac cgg ctc tgt gac aag tac ggc ctt tac gtc att gat gaa 3097
      286 Leu Phe Tyr Arg Leu Cys Asp Lys Tyr Gly Leu Tyr Val Ile Asp Glu
W--> 287                980                985                990
      289 gct aac ctg gaa agc cac ggc acc tgg gaa aaa gtg ggg ggg cac gaa 3145
      290 Ala Asn Leu Glu Ser His Gly Thr Trp Glu Lys Val Gly Gly His Glu
W--> 291                995                1000                1005
      293 gat cct agc ttc aat gtt cca ggc gat gac cag cat tgg ctg gga gcc 3193
      294 Asp Pro Ser Phe Asn Val Pro Gly Asp Asp Gln His Trp Leu Gly Ala
W--> 295                1010                1015                1020
      297 agc tta tcc cgg gtg aag aac atg atg gct cgg gac aag aac cat gct 3241
      298 Ser Leu Ser Arg Val Lys Asn Met Met Ala Arg Asp Lys Asn His Ala
W--> 299                1025                1030                1035
      301 tca atc ctg atc tgg tct tta ggc aat gag tct tac gcc ggc act gtc 3289
      302 Ser Ile Leu Ile Trp Ser Leu Gly Asn Glu Ser Tyr Ala Gly Thr Val
W--> 303 1040                1045                1050                1055
      305 ttt gcc caa atg gct gat tac gtc cgg aag gct gat ccg acc cgg gtt 3337
      306 Phe Ala Gln Met Ala Asp Tyr Val Arg Lys Ala Asp Pro Thr Arg Val
W--> 307                1060                1065                1070
      309 cag cac tat gaa ggg gtg acc cac aac cgg aag ttt gac gac gcc acc 3385
      310 Gln His Tyr Glu Gly Val Thr His Asn Arg Lys Phe Asp Asp Ala Thr
W--> 311                1075                1080                1085
      313 cag att gaa agc cgg atg tat gct ccg gcc aag gta att gaa gaa tac 3433
      314 Gln Ile Glu Ser Arg Met Tyr Ala Pro Ala Lys Val Ile Glu Glu Tyr
W--> 315                1090                1095                1100
      317 ttg acc aat aaa cca gcc aag cca ttt atc tca gtt gaa tac gct cac 3481
      318 Leu Thr Asn Lys Pro Ala Lys Pro Phe Ile Ser Val Glu Tyr Ala His
W--> 319                1105                1110                1115
      321 gcc atg ggc aac tcc gtc ggt gac ctg gcc gcc tac acg gcc ctg gaa 3529
      322 Ala Met Gly Asn Ser Val Gly Asp Leu Ala Ala Tyr Thr Ala Leu Glu
W--> 323 1120                1125                1130                1135
      325 aaa tac ccc cac tac cag ggc ggc ttc atc tgg gac tgg att gac caa 3577
      326 Lys Tyr Pro His Tyr Gln Gly Gly Phe Ile Trp Asp Trp Ile Asp Gln
W--> 327                1140                1145                1150

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VERIFICATION SUMMARY

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TIME: 11:43:19

Input Set : A:\PTO.txt

Output Set: N:\CRF3\04042001\I700687.raw

L:3 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:4 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:5 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:6 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:0 M:201 W: Mandatory field data missing, APPLICANT:
L:13 M:270 C: Current Application Number differs, Replaced Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:187 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:191 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:195 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:199 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:203 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:207 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:211 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:215 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:219 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:223 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:227 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:231 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:235 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:239 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:243 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:247 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:251 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:255 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:263 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:267 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:271 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:275 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:279 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
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L:287 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
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L:295 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:299 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
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L:311 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:315 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:319 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
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L:331 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:335 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:339 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:343 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:347 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/700,687

DATE: 04/04/2001

TIME: 11:43:19

Input Set : A:\PTO.txt

Output Set: N:\CRF3\04042001\I700687.raw

L:351 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
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L:359 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:363 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:367 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:371 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:375 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:379 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:383 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

PCT09

RAW SEQUENCE LISTING

DATE: 04/16/2001

PATENT APPLICATION: US/09/700,687

TIME: 13:23:16

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\04162001\I700687.raw

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2 <110> APPLICANT: GENDRE, Francois
3   BENBADIS, Laurent
4   BRIGNON, Pierre
5   COMPAGNIE GERVAIS DANONE
7 <120> TITLE OF INVENTION: MUTANT LACTOBACILLUS BULGARICUS STRAINS FREE
8   FROM BETA-GALACTOSIDASE ACTIVITY
10 <130> FILE REFERENCE: MJPCb191/143
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/700,687
C--> 13 <141> CURRENT FILING DATE: 2000-11-17
15 <150> PRIOR APPLICATION NUMBER: FR9806456
16 <151> PRIOR FILING DATE: 1998-05-22
18 <160> NUMBER OF SEQ ID NOS: 3
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 5059
24 <212> TYPE: DNA
25 <213> ORGANISM: Lactobacillus bulgaricus
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (122)..(1873)
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (1877)..(4519)
35 <400> SEQUENCE: 1
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38 tctgtcaacc tactttatcg tcttcgtcac caccacctc tttaatgccg gtgaccacaa 120
40 g'atg atc ttt atc atc acc aac ttg atc acc gcc atc cgg atc ggg gaa 169
41 Met Ile Phe Ile Ile Thr Asn Leu Ile Thr Ala Ile Arg Ile Gly Glu
42   1           5           10           15
44 gtc ctg ctc gac ccc ttg atc ggt aac gcc atc gac cgg acc gaa agc 217
45 Val Leu Leu Asp Pro Leu Ile Gly Asn Ala Ile Asp Arg Thr Glu Ser
46           20           25           30
48 cgg tgg ggg aag ttc aag ccc tgg gtt gtg ggc ggg ggg atc atc agc 265
49 Arg Trp Gly Lys Phe Lys Pro Trp Val Val Gly Gly Gly Ile Ile Ser
50           35           40           45
52 tca tta gcc ctc tta gcc ctc ttt acc gac ttt ggc ggc att aac caa 313
53 Ser Leu Ala Leu Leu Ala Leu Phe Thr Asp Phe Gly Gly Ile Asn Gln
54           50           55           60
56 agc aac ccc gtt gtt tac tta gta atc ttc ggt att gtt tac ttg att 361
57 Ser Asn Pro Val Val Tyr Leu Val Ile Phe Gly Ile Val Tyr Leu Ile
58 65           70           75           80
60 atg gat atc ttc tac tca ttt aaa gac act ggc ttc tgg gcc atg atc 409
61 Met Asp Ile Phe Tyr Ser Phe Lys Asp Thr Gly Phe Trp Ala Met Ile
62           85           90           95
64 ccg gcc ttg tcc ctg gat tcc cgg gaa aga gag aag acc tcc acc ttc 457
65 Pro Ala Leu Ser Leu Asp Ser Arg Glu Arg Glu Lys Thr Ser Thr Phe
66           100           105           110

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/700,687

DATE: 04/16/2001

TIME: 13:23:16

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\04162001\I700687.raw

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68 gcc aga gtc ggc tcc acc atc ggg gcc aac ctg gtc ggg gta gtc atc 505
69 Ala Arg Val Gly Ser Thr Ile Gly Ala Asn Leu Val Gly Val Val Ile
70      115      120      125
72 acc cca atc atc ctc ttc ttc tcg gcc agc aag gcc aac ccc aac ggg 553
73 Thr Pro Ile Ile Leu Phe Phe Ser Ala Ser Lys Ala Asn Pro Asn Gly
74      130      135      140
76 gat aag cag ggc tgg ttc ttc ttt gcc ttg atc gtg gcc att gtc ggc 601
77 Asp Lys Gln Gly Trp Phe Phe Phe Ala Leu Ile Val Ala Ile Val Gly
78 145      150      155      160
80 atc ttg acc tca att acc gtt ggt ctt ggt act cac gaa gta aaa tcc 649
81 Ile Leu Thr Ser Ile Thr Val Gly Leu Gly Thr His Glu Val Lys Ser
82      165      170      175
84 gcc ctg cgg gaa agc aat gaa aag acc act ttg aag cag gtc ttt aag 697
85 Ala Leu Arg Glu Ser Asn Glu Lys Thr Thr Leu Lys Gln Val Phe Lys
86      180      185      190
88 gtc ctg ggg caa aac gac cag ctc ctc tgg ctg gcc ttt gcc tac tgg 745
89 Val Leu Gly Gln Asn Asp Gln Leu Leu Trp Leu Ala Phe Ala Tyr Trp
90      195      200      205
92 ttt tac ggc ctg ggt atc aac acc ctg aac gct ctg caa ctt tac tac 793
93 Phe Tyr Gly Leu Gly Ile Asn Thr Leu Asn Ala Leu Gln Leu Tyr Tyr
94      210      215      220
96 ttc tca tac atc tta ggc gat gcc cgc ggc tac agc ctg ctt tac acc 841
97 Phe Ser Tyr Ile Leu Gly Asp Ala Arg Gly Tyr Ser Leu Leu Tyr Thr
98 225      230      235      240
100 atc aac acc ttt gtc ggt tta atc tct gca tcc ttc ttc cca tca ctg 889
101 Ile Asn Thr Phe Val Gly Leu Ile Ser Ala Ser Phe Phe Pro Ser Leu
102      245      250      255
104 gcc aag aag ttc aac aga aat cgc ctc ttc tac gcc tgc atc gcg gtg 937
105 Ala Lys Lys Phe Asn Arg Asn Arg Leu Phe Tyr Ala Cys Ile Ala Val
106      260      265      270
108 atg ctg tta ggg atc ggg gtc ttc tcc gtg gcc agc ggt tct ctg gcc 985
109 Met Leu Leu Gly Ile Gly Val Phe Ser Val Ala Ser Gly Ser Leu Ala
110      275      280      285
112 ctg tcc ctt gtt ggg gca gaa ttc ttc ttt att ccg cag cct ctg gcc 1033
113 Leu Ser Leu Val Gly Ala Glu Phe Phe Phe Ile Pro Gln Pro Leu Ala
114      290      295      300
116 ttc ctg gtc gtt ttg atg atc atc tct gac gct gtt gaa tac ggc cag 1081
117 Phe Leu Val Val Leu Met Ile Ile Ser Asp Ala Val Glu Tyr Gly Gln
118 305      310      315      320
120 ctg aaa act ggc cac aga gac gaa gct ttg acc ctg tct gtc cgg cca 1129
121 Leu Lys Thr Gly His Arg Asp Glu Ala Leu Thr Leu Ser Val Arg Pro
122      325      330      335
124 ttg gtc gat aag ctg ggc ggg gcc ttg tcc aac tgg ttt gtt tcc ttg 1177
125 Leu Val Asp Lys Leu Gly Gly Ala Leu Ser Asn Trp Phe Val Ser Leu
126      340      345      350
128 att gcc tta act gcc ggc atg acc act ggg gcg act gcc tca aca att 1225
129 Ile Ala Leu Thr Ala Gly Met Thr Thr Gly Ala Thr Ala Ser Thr Ile
130      355      360      365
132 aca gct cat ggc cag atg gtc ttc aag tta gct atg ttt gcc tta ccg 1273

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/700,687

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Input Set : A:\Cpg.pto

Output Set: N:\CRF3\04162001\I700687.raw

133	Thr	Ala	His	Gly	Gln	Met	Val	Phe	Lys	Leu	Ala	Met	Phe	Ala	Leu	Pro	
134		370					375					380					
136	gca	gtc	atg	ctc	ttg	atc	gct	gtt	tct	att	ttc	gcc	aaa	aag	gtc	ttc	1321
137	Ala	Val	Met	Leu	Leu	Ile	Ala	Val	Ser	Ile	Phe	Ala	Lys	Lys	Val	Phe	
138	385					390					395					400	
140	ttg	act	gaa	gaa	aag	cac	gcg	gaa	atc	gtc	gac	cag	ctg	gaa	act	caa	1369
141	Leu	Thr	Glu	Glu	Lys	His	Ala	Glu	Ile	Val	Asp	Gln	Leu	Glu	Thr	Gln	
142					405					410						415	
144	ttc	agc	caa	agc	cat	gcc	caa	aag	ccg	gcg	caa	gct	gaa	agc	ttc	act	1417
145	Phe	Ser	Gln	Ser	His	Ala	Gln	Lys	Pro	Ala	Gln	Ala	Glu	Ser	Phe	Thr	
146				420					425					430			
148	ttg	gcc	agc	cca	gtc	tcc	gga	caa	tta	atg	aac	ctg	gac	atg	gtt	gac	1465
149	Leu	Ala	Ser	Pro	Val	Ser	Gly	Gln	Leu	Met	Asn	Leu	Asp	Met	Val	Asp	
150			435						440					445			
152	gac	ccg	gtc	ttt	gcc	gac	aaa	aag	tta	ggc	gac	ggc	ttt	gcc	ctg	gtg	1513
153	Asp	Pro	Val	Phe	Ala	Asp	Lys	Lys	Leu	Gly	Asp	Gly	Phe	Ala	Leu	Val	
154		450					455							460			
156	cca	gca	gac	ggg	aag	gtc	tac	gcg	cca	ttt	gcc	ggg	act	gtc	cgc	cag	1561
157	Pro	Ala	Asp	Gly	Lys	Val	Tyr	Ala	Pro	Phe	Ala	Gly	Thr	Val	Arg	Gln	
158	465					470				475						480	
160	ctg	gcc	aag	acc	cgg	cac	tcc	atc	gtc	ctg	gaa	aat	gaa	cat	ggg	gtc	1609
161	Leu	Ala	Lys	Thr	Arg	His	Ser	Ile	Val	Leu	Glu	Asn	Glu	His	Gly	Val	
162				485						490						495	
164	ttg	gtc	ttg	att	cac	ctt	ggc	ctg	ggc	acg	gtc	aaa	tta	aac	ggg	act	1657
165	Leu	Val	Leu	Ile	His	Leu	Gly	Leu	Gly	Thr	Val	Lys	Leu	Asn	Gly	Thr	
166			500						505					510			
168	ggc	ttt	gtc	agc	tat	gtt	gaa	gag	ggc	agc	cag	gta	gaa	gcc	ggc	cag	1705
169	Gly	Phe	Val	Ser	Tyr	Val	Glu	Glu	Gly	Ser	Gln	Val	Glu	Ala	Gly	Gln	
170			515						520					525			
172	cag	atc	ctg	gaa	ttc	tgg	gac	ccg	gcg	atc	aag	cag	gcc	aag	ctg	gac	1753
173	Gln	Ile	Leu	Glu	Phe	Trp	Asp	Pro	Ala	Ile	Lys	Gln	Ala	Lys	Leu	Asp	
174		530					535							540			
176	gac	acg	gta	atc	gtg	acc	gtc	atc	aac	agc	gaa	act	ttc	gca	aat	agc	1801
177	Asp	Thr	Val	Ile	Val	Thr	Val	Ile	Asn	Ser	Glu	Thr	Phe	Ala	Asn	Ser	
178	545					550					555					560	
180	cag	atg	ctc	ttg	ccg	atc	ggc	cac	agc	gtc	caa	gcc	ctg	gat	gat	gta	1849
181	Gln	Met	Leu	Leu	Pro	Ile	Gly	His	Ser	Val	Gln	Ala	Leu	Asp	Asp	Val	
182				565						570						575	
184	ttc	aag	tta	gaa	ggg	aag	aat	tag	aaa	atg	agc	aat	aag	tta	gta	aaa	1897
185	Phe	Lys	Leu	Glu	Gly	Lys	Asn			Met	Ser	Asn	Lys	Leu	Val	Lys	
W--> 186			580							585						590	
188	gaa	aaa	aga	gtt	gac	cag	gca	gac	ttg	gcc	tgg	ctg	act	gac	ccg	gaa	1945
189	Glu	Lys	Arg	Val	Asp	Gln	Ala	Asp	Leu	Ala	Trp	Leu	Thr	Asp	Pro	Glu	
W--> 190			595						600					605			
192	gtt	tac	gaa	gtc	aat	aca	att	ccc	ccg	cac	tcc	gac	cat	gag	tcc	ttc	1993
193	Val	Tyr	Glu	Val	Asn	Thr	Ile	Pro	Pro	His	Ser	Asp	His	Glu	Ser	Phe	
W--> 194			610					615						620			
196	caa	agc	cag	gaa	gaa	ctg	gag	gag	ggc	aag	tcc	agt	tta	gtg	cag	tcc	2041
197	Gln	Ser	Gln	Glu	Glu	Leu	Glu	Glu	Gly	Lys	Ser	Ser	Leu	Val	Gln	Ser	

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/700,687

DATE: 04/16/2001

TIME: 13:23:16

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\04162001\I700687.raw

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W--> 198      625      630      635
      200 ctg gac ggg gac tgg ctg att gac tac gct gaa aac ggc cag gga cca 2089
      201 Leu Asp Gly Asp Trp Leu Ile Asp Tyr Ala Glu Asn Gly Gln Gly Pro
W--> 202 640      645      650      655
      204 gtc aac ttc tat gca gaa gac ttt gac gat agc aat ttt aag tca gtc 2137
      205 Val Asn Phe Tyr Ala Glu Asp Phe Asp Asp Ser Asn Phe Lys Ser Val
W--> 206      660      665      670
      208 aaa gta ccc ggc aac ctg gaa ctg caa ggc ttt ggc cag ccc cag tat 2185
      209 Lys Val Pro Gly Asn Leu Glu Leu Gln Gly Phe Gly Gln Pro Gln Tyr
W--> 210      675      680      685
      212 gtc aac gtc caa tat cca tgg gac ggc agt gag gag att ttc ccg ccc 2233
      213 Val Asn Val Gln Tyr Pro Trp Asp Gly Ser Glu Glu Ile Phe Pro Pro
W--> 214      690      695      700
      216 caa att cca agc aaa aat ccg ctc gct tct tat gtc aga tac ttt gac 2281
      217 Gln Ile Pro Ser Lys Asn Pro Leu Ala Ser Tyr Val Arg Tyr Phe Asp
W--> 218      705      710      715
      220 ctg gat gaa gct ttc tgg gac aag gaa gtc agc ttg aag ttt gac ggg 2329
      221 Leu Asp Glu Ala Phe Trp Asp Lys Glu Val Ser Leu Lys Phe Asp Gly
W--> 222 720      725      730      735
      224 gcg gca aca gcc atc tat gtc tgg ctg aac ggc cac ttc gtc ggc tac 2377
      225 Ala Ala Thr Ala Ile Tyr Val Trp Leu Asn Gly His Phe Val Gly Tyr
W--> 226      740      745      750
      228 ggg gaa gac tcc ttt acc cca agc gag ttt atg gtt acc aag ttc ctc 2425
      229 Gly Glu Asp Ser Phe Thr Pro Ser Glu Phe Met Val Thr Lys Phe Leu
W--> 230      755      760      765
      232 aag aaa gaa aat aac cgc ctg gca gtg gct ctc tac aag tat tct tcc 2473
      233 Lys Lys Glu Asn Asn Arg Leu Ala Val Ala Leu Tyr Lys Tyr Ser Ser
W--> 234      770      775      780
      236 gcc tcc tgg ctg gaa gac cag gac ttc tgg cgc atg tct ggt ttg ttc 2521
      237 Ala Ser Trp Leu Glu Asp Gln Asp Phe Trp Arg Met Ser Gly Leu Phe
W--> 238      785      790      795
      240 aga tca gtg act ctt cag gcc aag ccg cgt ctg cac ttg gag gac ctt 2569
      241 Arg Ser Val Thr Leu Gln Ala Lys Pro Arg Leu His Leu Glu Asp Leu
W--> 242 800      805      810      815
      244 aag ctt acg gcc agc ttg acc gat aac tac caa aaa gga aag ctg gaa 2617
      245 Lys Leu Thr Ala Ser Leu Thr Asp Asn Tyr Gln Lys Gly Lys Leu Glu
W--> 246      820      825      830
      248 gtc gaa gcc aat att gcc tac cgc ttg cca aat gcc agc ttt aag ctg 2665
      249 Val Glu Ala Asn Ile Ala Tyr Arg Leu Pro Asn Ala Ser Phe Lys Leu
W--> 250      835      840      845
      252 gaa gtg cgg gat agt gaa ggt gac ttg gtt gct gaa aag ctg ggc cca 2713
      253 Glu Val Arg Asp Ser Glu Gly Asp Leu Val Ala Glu Lys Leu Gly Pro
W--> 254      850      855      860
      256 atc aga agc gag cag ctg gaa ttc act ctg gct gat ttg cca gta gct 2761
      257 Ile Arg Ser Glu Gln Leu Glu Phe Thr Leu Ala Asp Leu Pro Val Ala
W--> 258      865      870      875
      260 gcc tgg agc gcg gaa aag cct aac ctt tac cag gtc cgc ctg tat tta 2809
      261 Ala Trp Ser Ala Glu Lys Pro Asn Leu Tyr Gln Val Arg Leu Tyr Leu
W--> 262 880      885      890      895

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/700,687

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TIME: 13:23:16

Input Set : A:\Cpg.pto

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264 tac cag gca ggc agc ctc tta gag gtt agc cgg cag gaa gtg ggt ttc 2857
265 Tyr Gln Ala Gly Ser Leu Leu Glu Val Ser Arg Gln Glu Val Gly Phe
W--> 266          900          905          910
268 cgc aac ttt gaa cta aaa gac ggg att atg tac ctt aac ggc cag cgg 2905
269 Arg Asn Phe Glu Leu Lys Asp Gly Ile Met Tyr Leu Asn Gly Gln Arg
W--> 270          915          920          925
272 atc gtc ttc aag ggg gcc aac cgg cac gaa ttt gac agt aag ttg ggc 2953
273 Ile Val Phe Lys Gly Ala Asn Arg His Glu Phe Asp Ser Lys Leu Gly
W--> 274          930          935          940
276 cgg gct atc aca gaa gag gat atg atc tgg gat atc aag acc atg aag 3001
277 Arg Ala Ile Thr Glu Glu Asp Met Ile Trp Asp Ile Lys Thr Met Lys
W--> 278          945          950          955
280 cga agc aac atc aat gct gtc cgc tgc tct cac tac ccg aac cag tcc 3049
281 Arg Ser Asn Ile Asn Ala Val Arg Cys Ser His Tyr Pro Asn Gln Ser
W--> 282 960          965          970          975
284 ctc ttt tac cgg ctc tgt gac aag tac ggc ctt tac gtc att gat gaa 3097
285 Leu Phe Tyr Arg Leu Cys Asp Lys Tyr Gly Leu Tyr Val Ile Asp Glu
W--> 286          980          985          990
288 gct aac ctg gaa agc cac ggc acc tgg gaa aaa gtg ggg ggg cac gaa 3145
289 Ala Asn Leu Glu Ser His Gly Thr Trp Glu Lys Val Gly Gly His Glu
W--> 290          995          1000          1005
292 gat cct agc ttc aat gtt cca ggc gat gac cag cat tgg ctg gga gcc 3193
293 Asp Pro Ser Phe Asn Val Pro Gly Asp Asp Gln His Trp Leu Gly Ala
W--> 294          1010          1015          1020
296 agc tta tcc cgg gtg aag aac atg atg gct cgg gac aag aac cat gct 3241
297 Ser Leu Ser Arg Val Lys Asn Met Met Ala Arg Asp Lys Asn His Ala
W--> 298          1025          1030          1035
300 tca atc ctg atc tgg tct tta ggc aat gag tct tac gcc ggc act gtc 3289
301 Ser Ile Leu Ile Trp Ser Leu Gly Asn Glu Ser Tyr Ala Gly Thr Val
W--> 302 1040          1045          1050          1055
304 ttt gcc caa atg gct gat tac gtc cgg aag gct gat ccg acc cgg gtt 3337
305 Phe Ala Gln Met Ala Asp Tyr Val Arg Lys Ala Asp Pro Thr Arg Val
W--> 306          1060          1065          1070
308 cag cac tat gaa ggg gtg acc cac aac cgg aag ttt gac gac gcc acc 3385
309 Gln His Tyr Glu Gly Val Thr His Asn Arg Lys Phe Asp Asp Ala Thr
W--> 310          1075          1080          1085
312 cag att gaa agc cgg atg tat gct ccg gcc aag gta att gaa gaa tac 3433
313 Gln Ile Glu Ser Arg Met Tyr Ala Pro Ala Lys Val Ile Glu Glu Tyr
W--> 314          1090          1095          1100
316 ttg acc aat aaa cca gcc aag cca ttt atc tca gtt gaa tac gct cac 3481
317 Leu Thr Asn Lys Pro Ala Lys Pro Phe Ile Ser Val Glu Tyr Ala His
W--> 318          1105          1110          1115
320 gcc atg ggc aac tcc gtc ggt gac ctg gcc gcc tac acg gcc ctg gaa 3529
321 Ala Met Gly Asn Ser Val Gly Asp Leu Ala Ala Tyr Thr Ala Leu Glu
W--> 322 1120          1125          1130          1135
324 aaa tac ccc cac tac cag ggc ggc ttc atc tgg gac tgg att gac caa 3577
325 Lys Tyr Pro His Tyr Gln Gly Gly Phe Ile Trp Asp Trp Ile Asp Gln
W--> 326          1140          1145          1150
328 gga ctg gaa aaa gac ggg cac ctg ctt tat ggg ggc gac ttc gat gac 3625

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VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:186 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:190 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:194 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:202 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:206 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:210 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:214 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:218 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:222 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:226 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:230 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:234 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:238 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:242 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:246 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:250 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:254 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:258 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:262 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:266 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:270 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:274 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:278 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:282 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:286 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:290 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:294 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:298 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:302 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:306 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:310 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:314 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:318 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:322 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:326 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:330 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:334 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:338 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:342 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:346 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:350 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:354 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:358 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:362 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:366 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/700,687

DATE: 04/16/2001

TIME: 13:23:17

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\04162001\I700687.raw

L:370 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:374 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:378 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:382 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1